

Query Match	9.6%;	Score 146.6;	DB 4;	Length 876;
Best Local Similarity	52.28;	Pred. No. 1.7e-41;		
Matches 385;	Conservative 0;	Mismatches 334;	Indels 18;	Gaps 2;
QY	ATTATTAAGCTGGGAGCTGGAGCTGTATAGACAGTCAACACGACCAAGTGTGGCTGGAC	870		
DB	ATTTTACATGGGATTTCACACTTTATGACCTTTCAAAGGTTACTTAAAGTGGGTTTAAAC	195		
QY	AAGACCTGATTTTGTGCTGTGCATGACGATTAAGCTCTGCTGTAATCCGCTCAGGAA	930		
DB	AAAGATTTGTTTGTCTCCCAAGTTGACGATTAAGTTGTCAATTTGCTGCTCTTAAT	255		
QY	GCTCTGCTTGGCTCATCCG-----ACAGTACTTCACTAAGCTGTATCAAGATGGTCCGT	984		
DB	GCATTGATTTGATTCTACCGTGGACCAACATTTGGCCGAGATTCTTTTTCATATGTTGGG	315		
QY	ATGTTTGAATGACGAGAAATTGGAAGCCTGGCTGGCCGAGAGCTGCATCCAACTTCATG	1044		
DB	TTGTTTGAATTAAGAGAAATTTGGCTCTCTCACTAACAAAGTGCTAGAGGTGAATTAAT	375		
QY	AGCAGTGCATAGAGCTATTACGGAAACCTTCTCACCACCAATTACGATCTTAAACGTGCTG	1104		
DB	GAATTAAGTTGTGACAGAGTGTGTGCATCTAATTTCTTAATCCGAAAGTTCTTGATATT	435		

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 03:55:19 ; Search time 961 Seconds
(without alignments)
10242.485 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602
Perfect score: 1530
Sequence: 1 atgacccaagaagatgtctt.....acaagaattgcagatttc 1530

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1530	100.0	1679	US-10-664-958-4
2	787.6	51.5	1916	US-10-664-958-2
3	787.6	51.5	3383	US-10-664-958-1
4	184.6	12.1	707	US-10-653-047-448
5	119.2	7.8	1656	US-10-425-114-11096
6	117.6	7.7	1807	US-10-425-114-3262
7	117.6	7.7	1948	US-10-425-115-5515

8	115.2	7.5	844	US-10-425-115-42258	Sequence 42258, A
9	109.2	7.1	1696	US-10-353-690-69	Sequence 69, Appl
10	109.2	7.1	1696	US-10-956-157-1776	Sequence 1776, Ap
11	109.2	7.1	2583	US-10-357-930-22225	Sequence 22225, A
12	109.2	7.1	2583	US-10-357-930-22225	Sequence 28083, A
13	108	7.1	1975	US-10-424-599-14244	Sequence 14244, A
14	95.4	6.2	1784	US-10-437-963-98779	Sequence 98779, A
15	86.6	5.7	3380	US-10-128-714-5416	Sequence 5416, Ap
16	86.6	5.7	3381	US-10-128-714-5416	Sequence 74, Appl
17	83.8	5.5	1117	US-10-767-792-74	Sequence 54577, A
18	82	5.4	844	US-10-425-115-54577	Sequence 54577, A
19	79.6	5.2	1284	US-10-148-414-8	Sequence 8, Appl1
20	78.2	5.1	637	US-10-767-701-6053	Sequence 6053, Ap
21	76.8	5.0	600	US-10-956-157-7011	Sequence 7011, Ap
22	76.4	5.0	681	US-10-283-978A-763	Sequence 763, App
23	70.2	4.6	544	US-10-425-115-82175	Sequence 82175, A
24	70	4.6	754	US-10-767-701-6113	Sequence 6113, Ap
25	69.2	4.5	1576	US-10-425-114-29546	Sequence 29546, A
26	66.6	4.4	607	US-10-021-323-4253	Sequence 4253, Ap
27	63.4	4.1	215	US-10-424-599-140276	Sequence 140276
28	62.6	4.1	489	US-09-732-627A-3018	Sequence 3018, Ap
29	61.4	4.0	583	US-10-425-115-101845	Sequence 101845, A
30	59.6	3.9	414	US-09-918-995-3652	Sequence 3652, Ap
31	59.6	3.9	421	US-09-918-995-4180	Sequence 4180, Ap
32	58.8	3.8	735	US-10-767-701-26797	Sequence 26797, A
33	54.8	3.6	385	US-09-918-995-8281	Sequence 8281, Ap
34	51.8	3.4	442	US-10-357-930-32748	Sequence 42647, A
35	50	3.3	571	US-10-021-323-4268	Sequence 4809, Ap
36	49.2	3.2	827	US-10-424-599-140279	Sequence 4268, Ap
37	48.8	3.2	463	US-10-357-930-32748	Sequence 140279, A
38	48.6	3.2	463	US-10-357-930-32748	Sequence 12589, A
39	48.6	3.2	463	US-10-357-930-32748	Sequence 33748, A
40	45.4	3.0	1236	US-10-156-761-4373	Sequence 4373, Ap
41	45.4	3.0	902	US-10-156-761-4373	Sequence 1, Appl
42	43.8	2.9	3662	US-10-320-797-205	Sequence 205, App
43	43.4	2.8	607	US-10-123-151-102	Sequence 102, App
44	43.4	2.8	607	US-10-146-731-102	Sequence 102, App
45	43.4	2.8	607	US-10-140-472-102	Sequence 102, App

ALIGNMENTS

RESULT 1
US-10-664-958-4
Sequence 4, Application US/10664958
Publication No. US20040219636A1
GENERAL INFORMATION:
APPLICANT: KOIBUCHI, KYOKO
APPLICANT: NINOMIYA, DAIKI
APPLICANT: KOTIMA, MARI
APPLICANT: UEDA, YOICHI
APPLICANT: MATSUMOTO, JUN-ICHI
APPLICANT: KITAMOTO, KATSUHIKO
TITLE OF INVENTION: NEW AMINOPEPTIDASE AND THE GENES THEREOF
FILE REFERENCE: 241461USOCONT
CURRENT APPLICATION NUMBER: US/10/664, 958
CURRENT FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: PCT/JP02/02476
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: JP 2001-078930
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: JP 2001-293348
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 1679
TYPE: DNA
ORGANISM: Aspergillus oryzae
FEATURE:
NAME/KEY: CDS
LOCATION: (73)..(1602)

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2005, 01:48:04 ; Search time 4629 Seconds
(without alignments)
12581.191 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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3: gb_hic.*
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9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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2	453.4	29.6	684 7	CO136018 EST830689
3	419.8	27.4	898 7	CO005654 EST793989
4	409.4	26.8	901 7	CO013013 EST801348
5	382.6	25.0	827 7	CO005655 EST793990
6	352	23.0	780 7	CO009866 EST798201
7	320.8	21.0	859 7	CO013014 EST801349
8	316.4	20.7	535 1	AT211309 O6D09a1.r
9	277.4	18.1	530 1	AT211331 O6D03a1.r
10	256.4	16.8	764 6	CD485799 CF083.1H0
11	247.6	16.2	759 6	CB903053 trlC032x1
12	247.4	16.2	691 7	CF873032 trlC032x1
13	231	15.1	768 9	CL558944 OB_Ba001
14	215	14.1	391 5	BQ499748 EST08973
15	211.2	13.8	828 2	BE643133
16	210.2	13.7	434 7	CN249799 EST015716
17	195.6	12.8	539 1	AT211330 O6D03a1.f
18	184.6	12.1	1030 7	CN248531 EST014438
19	171.6	11.2	758 7	CN240819 EST006682
20	167.4	10.9	915 7	CF883173 trlC032x1
21	159.2	10.4	519 5	BQ503674 EST12904
22	154.4	10.1	734 9	CF883059 trlC032x1
23	153	10.0	571 9	CL559297 OB_Ba001
24	153	10.0	580 7	CN249701 EST015620

25	143.4	9.4	463	2	BF252877	BF252877 EST420140
26	140.2	9.2	974	7	CNS06Y0Z	AL421305 T3 end of
27	136.8	8.9	268	7	CO009867	CO009867 EST798202
28	133.8	8.7	441	5	BQ502774	BQ502774 EST12004
29	126.2	8.2	641	7	CK907937	CK907937 rhzma0.00
30	121	7.9	780	7	CO019776	CO019776 EST815869
31	118.2	7.7	584	8	BZ293586	BZ293586 CG0412.r1
32	114.4	7.5	1422	9	AY399515	AY399515 Mus muscu
33	112.8	7.4	2469	9	AK038646	AK038646 Mus muscu
34	111.8	7.3	885	7	CF821438	CF821438 EST69820
35	109.2	7.1	1509	9	AY399513	AY399513 Homo sapi
36	109.2	7.1	1560	3	CNS0A1BQ	BX829510 Arabidops
37	107.8	7.0	2835	3	AK052001	AK052001 Mus muscu
38	107.6	7.0	1319	3	CR602255	CR602255 full-1eng
39	107.6	7.0	1527	3	CR601156	CR601156 full-1eng
40	107.6	7.0	1528	3	CR620845	CR620845 full-1eng
41	107.6	7.0	1544	3	CR605917	CR605917 full-1eng
42	107.6	7.0	1593	3	CR608875	CR608875 full-1eng
43	107.6	7.0	1594	3	CR593910	CR593910 full-1eng
44	107.6	7.0	1602	3	CR607064	CR607064 full-1eng
45	107.6	7.0	1622	3	CR611309	CR611309 full-1eng

ALIGNMENTS

RESULT 1
LOCUS CO150272 636 bp mRNA linear EST 17-JUN-2004
DEFINITION EST825325 Aspergillus flavus Normalized cDNA Expression Library
Aspergillus flavus cDNA clone NAGEB35 5' end, mRNA sequence.
CO150272
CO150272.1 GI:48904273

SOURCE

Aspergillus flavus
Aspergillus flavus

REFERENCE

1 (bases 1 to 636)
Yu, J., Whitelaw, C.A., Nierman, W.C., Bhatnagar, D. and Cleveland, T.B.
Aspergillus flavus expressed sequence tags for identification of genes with putative roles in aflatoxin contamination of crops
FEMS Microbiol. Lett. (2004) In press

JOURNAL

Contact: Yu J
Food and Feed Safety Research Unit
USDA/ARS, Southern Regional Research Center
1100 Robert E. Lee Boulevard, New Orleans, LA 70124, USA
Tel: 504 286 4405
Fax: 504 286 4419

COMMENT

Email: jiyu@arcc.ars.usda.gov
Contact Dr. Yu at USDA/ARS SRRC (jiyu@arcc.ars.usda.gov) for clone information
PCR Primers
FORWARD: M13F
BACKWARD: M13R
Seq primer: M13 Forward
POLYA-No.

FEATURES

Source

Location/Qualifiers
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/strain="NRRL 3357"

/db_xref="taxon:5059"

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/sex="asexual mycelia"

/cell_type="mycelia"

/dev_stage="developmental stages from 18 to 96 hours"

/lab_host="E. coli DH10B T1 resistant cells"

/clone_id="Aspergillus flavus Normalized cDNA Expression Library"

/note="Vector: pBlueScript (SK+) (Stratagene), antibiotic selection marker: Carbenicillin; Site 1: NotI, at the 5 prime end; Site 2: BcoRI, at the 3 prime end; This

PS Claim 1; Page 45-49; 61pp; Japanese.

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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 11, 2005, 15:11:49 ; Search time 125.5 seconds
(without alignments)
9617.214 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1777461 seqs, 394431504 residues
Total number of hits satisfying chosen parameters: 3554922

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2626	94.3	510	16	US-10-664-958-5
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4	831.5	29.5	565	15	US-10-425-114-47233
5	821.5	29.5	487	15	US-10-425-114-47233
6	814	29.2	475	16	US-10-425-115-190178
7	806.5	29.0	478	16	US-10-425-115-190178
8	737.5	26.5	425	15	US-10-353-690-70
9	676	24.3	478	15	US-10-148-414-9
10	553.5	19.9	491	15	US-10-424-599-283118
11	498.5	17.9	420	9	US-09-804-073-2
12	498.5	17.9	441	9	US-09-738-626-5156
13	486.5	17.5	432	14	US-10-156-761-11923
14	434.5	15.6	253	16	US-10-425-115-239240
15	406	14.6	240	16	US-10-425-115-239240
16	352	12.6	161	16	US-10-767-701-37617
17	349.5	12.6	258	16	US-10-425-114-55505
18	310.5	11.2	226	16	US-10-767-701-58361
19	300.5	10.8	173	16	US-10-767-701-37617
20	276.5	9.9	155	16	US-10-425-115-286508
21	268.5	9.6	181	16	US-10-425-115-286838
22	266.5	9.6	160	16	US-10-437-963-191727
23	254	9.1	179	16	US-10-767-701-36045
24	250	9.0	138	15	US-10-424-599-283121
25	244.5	8.8	154	16	US-10-437-963-116670
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27	192.5	6.9	165	16	US-10-437-963-120177
28	179.5	6.4	114	16	US-10-437-963-120177
29	148.5	5.3	97	15	US-10-424-599-274525
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34	118	4.2	519	15	US-10-369-493-24338
35	118	4.2	519	16	US-10-451-467A-774
36	117	4.2	19723	15	US-10-084-846A-5
37	116	4.2	19695	15	US-10-084-846A-3
38	115.5	4.1	463	16	US-10-437-963-109124
39	115	4.1	487	16	US-10-437-963-117896
40	111.5	4.0	6842	15	US-10-461-194-131
41	111	4.0	2442	13	US-10-109-886-10
42	111	4.0	2442	16	US-10-473-127-631
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45	111	4.0	2442	16	US-10-473-127-647

ALIGNMENTS

RESULT 1
US-10-664-958-5
; Sequence 5, Application US/10664958
; Publication No. US20040219636A1
; GENERAL INFORMATION:
; APPLICANT: KOJIBUCHI, KYOKO
; APPLICANT: NINOMIYA, DAIKI
; APPLICANT: KOJIMA, MARI
; APPLICANT: UEDA, YOICHI
; APPLICANT: MARUYAMA, JUN-ICHI
; APPLICANT: KITAMOTO, KATSUHIKO
; TITLE OF INVENTION: NEW AMINOPEPTIDASE AND THE GENES THEREOF
; FILE REFERENCE: 241461US0CONT
; CURRENT APPLICATION NUMBER: US/10/664,958
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: JP 2001-078930
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: JP 2001-293348

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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 11, 2005, 14:45:13 ; Search time 37 Seconds
(without alignments)
6173.679 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602
Perfect score: 2784
Sequence: 1 atgaccacaaagagtgctc.....acaaggaattgcagatttc 1530

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2_1/USFPO_sepol_p/US10664958/r/nat.10092005.173356.1993/app_query.fasta_1.1671
-DB=Issued_Patents_AA -QFRT=fastan -SUFFIX=top20.ral -MINMATCH=0.1 -LOOPT=0
-LOOEXT=0 -UNITS=Dits -START=1 -END=1 -MATRIX=blowsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=pcio -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10664958 @cgn 1.1.33 @nat.10092005.173356.1993 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents AA:

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTCIS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1013.5	36.4	514	US-09-538-092-495	Sequence 495, App
2	811.5	29.1	487	US-09-525-046-2	Sequence 2, Appl
3	737.5	26.5	471	US-09-071-709-4	Sequence 4, Appl
4	737.5	26.5	471	US-09-160-494-2	Sequence 2, Appl
5	732.5	26.3	471	US-09-160-494-6	Sequence 6, Appl
6	681.5	24.5	485	US-09-252-991A-21636	Sequence 21636, A
7	645.5	23.2	470	US-09-248-796A-19473	Sequence 19473, A
8	640	23.0	470	US-09-071-709-12	Sequence 12, Appl
9	559.5	20.1	459	US-09-160-494-4	Sequence 4, Appl
10	542.5	19.5	447	US-08-311-731A-246	Sequence 246, App
11	498.5	17.9	420	US-09-602-777A-110	Sequence 110, App
12	473	17.0	291	US-09-248-796A-19474	Sequence 19474, A

13	451.5	16.2	318	US-09-248-796A-19475	Sequence 19475, A
14	448.5	16.1	249	US-09-248-796A-19487	Sequence 19487, A
15	412	14.8	225	US-09-248-796A-19486	Sequence 19486, A
16	244.5	8.8	283	US-09-248-796A-19476	Sequence 19476, A
17	141	5.1	752	US-09-252-991A-21724	Sequence 21724, A
18	119	4.3	1093	US-09-252-991A-21827	Sequence 21827, A
19	112.5	4.0	629	US-09-252-991A-17150	Sequence 17150, A
20	111	4.0	2442	US-09-514-247A-10	Sequence 1370, Ap
21	111	4.0	2442	US-09-538-092-1370	Sequence 16, Appl
22	109	3.9	648	US-09-437-687A-16	Sequence 16, Appl
23	109	3.9	648	US-10-263-250-16	Sequence 16, Appl
24	109	3.9	1220	US-08-158-232-43	Sequence 43, Appl
25	109	3.9	1220	US-08-611-928-43	Sequence 43, Appl
26	109	3.9	1220	US-09-173-891-43	Sequence 43, Appl
27	108.5	3.9	620	US-08-889-092-2	Sequence 2, Appl
28	107.5	3.9	2090	US-09-538-092-1081	Sequence 1081, Ap
29	107.5	3.9	2120	US-09-949-016-9768	Sequence 9768, Ap
30	106.5	3.8	654	US-09-437-687A-2	Sequence 2, Appl
31	106.5	3.8	654	US-10-263-250-2	Sequence 2, Appl
32	105.5	3.8	620	US-08-419-652-7	Sequence 7, Appl
33	105.5	3.8	898	US-08-465-995A-4	Sequence 4, Appl
34	105.5	3.8	898	US-08-465-994C-4	Sequence 4, Appl
35	105.5	3.8	898	US-08-966-145-4	Sequence 4, Appl
36	105.5	3.8	920	US-08-101-593-4	Sequence 4, Appl
37	105.5	3.8	1001	US-07-797-556-6	Sequence 6, Appl
38	105.5	3.8	1001	US-07-943-843-2	Sequence 2, Appl
39	105.5	3.8	1001	US-08-347-003-2	Sequence 2, Appl
40	105.5	3.8	1097	US-07-943-843-6	Sequence 6, Appl
41	105.5	3.8	1097	US-08-347-003-6	Sequence 6, Appl
42	105.5	3.8	1097	US-09-949-016-6209	Sequence 6209, Ap
43	105.5	3.8	1119	US-09-949-016-10081	Sequence 10081, A
44	105.5	3.8	1385	US-09-252-991A-21919	Sequence 21919, A
45	104.5	3.8	898	US-08-465-995A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-538-092-495
Sequence 495, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Tracy A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538, 092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CnapatSeqFormatter Version 0.9
SEQ ID NO 495
LENGTH: 514
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
NAME/KEY: misc.feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number YK1A03C
US-09-538-092-495

Alignment Scores:
Pred. No.: 8.21e-96
Score: 1013.50
Percent Similarity: 60.04%
Best Local Similarity: 42.44%
Query Match: 36.40%
DB: 4
Gaps: 8

US-10-664-958-4_COPY_73_1602 (1-1530) * US-09-538-092-495 (1-514)

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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 11, 2005, 05:18:03 ; Search time 158.5 Seconds
(without alignments)
9886.198 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602

Perfect score: 2784
Sequence: 1 atgacccaagaagagtgctc.....acaaggaattgcagatttc 1530

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p model -DEV=xl
-Q=/cgn2_1/USFWO_spool_p/US1066958/runat_10092005_173355_1973/app_query.fasta_1.1671
-DB=uniprot_03 -QFMT=fastan -SUPFIX=top20.rup -MINMATCH=40.1 -LOOPEL=0
-LIST=45 -UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi
-MODE=LOCAL -OUTFMT=plc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRB=US1066958_QCGN_1.1_153 @runat_10092005_173355_1973 -NCP=6 -ICP=3
-NO_MAP -LARGEOUTRY -NB3_SCORES=0 -WAIT -DSPBLCK=100 -LONGLOC
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1528	54.9	535	2	Q9H85	Q9H85 neurospora
2	1174	42.2	493	2	O6CCD1	O6ccdi yarrowia li
3	1040	37.4	509	2	O6FMF2	O6fmf2 candida gla
4	1034.5	37.2	519	2	O6CK48	O6ck48 kluyveromyc
5	1013.5	36.4	514	1	AMPL_YEAST	PL4904 sacharomyc
6	1006	36.1	506	2	O6BHT6	O6bjh6 debaryomyc
7	998	35.8	469	2	O6C022	O6c022 yarrowia li
8	907.5	32.6	498	2	O75DQ2	O75dq2 ashyba goss
9	883.5	31.7	476	2	O6CFM9	O6cfm9 yarrowia li
10	867	31.1	495	2	O96TK5	O96tk5 coccidioid
11	866.5	31.1	499	2	O6CMCS	O6cmcs kluyveromyc
12	862.5	31.0	523	2	O6BKU6	O6bku6 debaryomyc
13	858	30.8	493	2	O6BHZ6	O6bhz6 debaryomyc
14	857	30.8	484	2	O6FRJ3	O6frj3 candida gla
15	856	30.7	484	2	O7RYK7	O7ryk7 neurospora
16	843	30.3	490	1	DNPE_YEAST	P38821 saccharomyc

17	814.5	29.3	467	1	DNPE_SCHPO	O36014 schizosacch
18	782.5	28.1	477	2	O9LSTO	O9lst0 arabidopsis
19	777.5	27.9	477	2	O8LFF32	O8lff32 arabidopsis
20	737.5	26.5	475	1	DNPE_HUMAN	O9uia0 homo sapien
21	737	26.5	525	2	O8SA06	O8sa06 oryza sativ
22	728.5	26.2	473	1	DNPE_MOUSE	O922w0 mus musculu
23	728.5	26.2	473	1	O8CAJ7	O8caj7 mus musculu
24	718	25.8	526	2	O9L226	O9l226 arabidopsis
25	714	25.6	526	2	O8GM19	O8gm19 arabidopsis
26	700.5	25.2	470	2	O8BPW9	O8bpw9 mus musculu
27	699.5	25.1	469	2	O803B5	O803b5 mus musculu
28	692	24.9	479	2	O6Q061	O6q061 xenopus lae
29	682	24.5	429	1	APER_PSEPK	O8em44 pseudomonas
30	677	24.3	429	1	APER_PSEAR	O9hyz3 pseudomonas
31	670	24.1	429	1	APER_PSESM	O97f4 pseudomonas
32	640	23.0	433	1	APER_CLOAB	O13087 caenorhabdi
33	640	23.0	470	1	DNPE_CABSL	O891c3 clostridium
34	627.5	22.5	430	2	O891C3	O891c3 clostridium
35	613.5	22.0	441	2	O9NV55	O9nv55 homo sapien
36	605	21.7	437	2	O6AL63	O6al63 desulfotale
37	582	20.9	430	2	O73PH0	O73ph0 treponema d
38	581	20.9	431	2	O8XMT1	O8xmt1 clostridium
39	560.5	20.1	429	2	O8RFD2	O8rfd2 fusobacteri
40	557	20.0	434	2	O820D1	O820d1 nitrosomona
41	552.5	19.8	429	2	O7P659	O7p659 fusobacteri
42	546	19.6	378	2	O9BS59	O9bs59 homo sapien
43	542.5	19.5	426	1	APER_MYCLE	O50022 mycobacteri
44	538.5	19.3	429	2	O6SG58	O6sg58 uncultured
45	502.5	18.0	428	2	O6AA87	O6aa87 propionibac

ALIGNMENTS

RESULT 1

Q9H85 PRELIMINARY, PRT, 535 AA.
AC Q9H85;
DT 01-MAR-2001 (TREMBL) 16, (last sequence update)
DT 01-MAR-2004 (TREMBL) 26, (last annotation update)
DE Related to aminopeptidase ysc1, vacuolar.
GN Name=B13020.180;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Altm V., Hohenstein J., Brandt P., Fartmann B., Holland R.,
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AL451015; CAC18208.1; .
DR GO; GO:0005773; C:vacuole; IEA.
DR GO; GO:0004250; P:aminopeptidase I activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR Interpro; IPR001948; Peptidase M18.
DR Pfam; PF02127; Peptidase M18; I.
DR PRINTS; PR00932; AMINOPEPTASE.
DR KX
DR AMINOPEPTIDASE.
SQ SEQUENCE 535 AA; 58137 MW; 469F22A535396798 CRC64;

Alignment Scores:
Pred. No.: 4.3e-102
Score: 1528.00
Percent Similarity: 72.35%
Best Local Similarity: 57.77%
Query Match: 54.89%
Matches: 305
Conservative: 77
Mismatch: 119
Gaps: 27
Gaps: 5

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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 11, 2005, 05:12:35 ; Search time 125 Seconds
(without alignments)
9467.694 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602
Perfect score: 2784
Sequence: 1 atgaccaaagagtgctcct.....acaagaattcgacagatttc 1530

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+np2_model -DEV=xl
-O=Cgnt_1_USPTO_epool_p/US1066958/runat_10092005_17354_1967/app_query.fasta_1.1671
-DB=4_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=top20.rag -MINMATCH=0.1 -LOOPT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10664958 @CGN_1_1_154 @runat_10092005_17354_1967 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2626	94.3	510	6	AAO19562
2	2112.5	75.9	519	6	AAO19561
3	1013.5	36.4	514	2	AAO5535
4	821.5	29.5	487	3	AAO26490
5	746	26.8	485	4	AAO93510
6	739	26.5	485	4	AAO94381
7	737.5	26.5	471	3	AAO17722
8	737.5	26.5	471	3	AAO17715
9	737.5	26.5	475	7	AAO31713
10	737.5	26.5	475	7	AAO31713

11	737.5	26.5	475	8	ABM80387
12	732.5	26.3	471	2	AAV29466
13	688	24.7	449	8	AD116362
14	681.5	24.5	485	7	ABO72890
15	678	24.4	428	4	AAU05191
16	640	23.0	470	3	AAO17723
17	613.5	22.0	441	4	AAO93327
18	560	20.1	407	8	ADP04194
19	559.5	20.1	459	2	AAV29465
20	558	20.0	499	8	ADP04193
21	542.5	19.5	447	7	ABO74497
22	502.5	18.0	428	4	AAU58862
23	502.5	18.0	428	6	AAO55381
24	499.5	17.9	315	3	AAO23766
25	499.5	17.9	321	4	AAO23765
26	498.5	17.9	420	4	AAO79977
27	498.5	17.9	420	5	ABO79402
28	498.5	17.9	441	4	AAO91402
29	356	12.8	267	4	AAO93839
30	174	6.2	163	3	AAO23767
31	141	5.1	752	7	ABO72978
32	124.5	4.5	94	5	ABO06629
33	120.5	4.3	925	7	ADMO5204
34	120.5	4.3	1688	4	ABO59327
35	119	4.3	1093	7	ABO73081
36	118.5	4.3	1938	6	ABO98398
37	118	4.2	519	5	ABO93208
38	118	4.2	519	8	AUS44008
39	117	4.2	346	8	ADN46314
40	116.5	4.2	1403	4	ABO60540
41	116	4.2	649	4	AAU52702
42	116	4.2	649	6	ABO49221
43	113.5	4.1	1770	8	ADN97110
44	113.5	4.1	2354	8	ADQ97650
45	112.5	4.0	629	7	ABO68404

ALIGNMENTS

RESULT 1	AAO19562	standard; protein; sig AA.
ID	AAO19562	standard; protein; sig AA.
AC	AAO19562;	
DT	23-OCT-2003	(revised)
DT	31-JAN-2003	(first entry)
XX		
DE	A nidulans aminopeptidase #2.	
XX		
KW	Aminopeptidase; protein digestion; seasoning; soy sauce; cooking sauce.	
XX		
OS	Emeticella nidulans.	
XX		
EN	WO200277223-A1.	
XX		
PD	03-OCT-2002.	
XX		
PF	15-MAR-2002; 2002WO-JP002476.	
XX		
PR	19-MAR-2001; 2001JP-00078930.	
PR	26-SEP-2001; 2001JP-00293348.	
XX		
PA	(AJIN) AJINOMOTO CO INC.	
XX		
PI	Kojibuchi K, Ninomiya D, Kojima M, Ueda Y, Maruyama J, Kitamoto K;	
XX	WPI, 2003-018923/01.	
DR	N-PSDB; AAL50169.	
XX		
PT	Novel Aspergillus nidulans-originated aminopeptidase and encoded gene,	
PT	capable of digesting hardly digestible peptides, applicable e.g. in	
PT	producing natural seasoning materials containing protein hydrolyzates	

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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 11, 2005, 14:11:55 ; Search time 41.5 Seconds
(without alignments)
7094.537 Million cell updates/sec

Title: US-10-664-958-4_COPY_73_1602

Perfect score: 2784

Sequence: 1 atgacacaaaggatgctcct.....acaaggaattcagagatttc 1530

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p model -DRV=xld
-O=/cgn2.1/USPTO_spool_p/US10664958/runat_10092005_173355_1981/app_query_fasta_1.1671
-DB=PIR_79 -OPMT=fastan -SUFFIX=top20.rpr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTPMT=pct -NORM=ext -HEAFSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10664958 @CCN 1.1 40 @runat_10092005_173355_1981 -NCPU=6 -ICPU=3
-NO_MAP -LARGEBUFFER -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGCLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1013.5	36.4	514	2	A33879
2	843	30.3	490	2	S48955
3	814.5	29.3	467	2	T38806
4	718	25.8	526	2	T48467
5	677	24.3	429	2	A83240
6	650.5	23.4	392	2	T43206
7	640	23.0	433	2	F96974
8	640	23.0	470	2	T15946
9	542.5	19.5	443	2	H87185
10	486	17.5	433	2	A70536
11	485.5	17.4	432	2	T36482
12	446.5	16.0	423	2	B70178
13	333	12.0	452	2	B72387
14	304.5	10.9	458	2	E70145

15	276.5	9.9	465	2	F97034	aspartyl aminopept
16	124.5	4.5	2152	2	T45583	hypothetical prote
17	420	4.3	528	2	I47141	gastric mucin (clo
18	118	4.2	519	1	S67286	probable aldehyde
19	117	4.2	1222	2	G59100	hypothetical prote
20	117	4.2	2232	2	T34434	hypothetical prote
21	115.5	4.1	553	2	T52362	hypothetical prote
22	115.5	4.1	1161	2	S57180	probable membrane
23	115	4.1	967	2	H85334	T2012.10 protein -
24	114.5	4.1	1299	2	T47182	hypothetical prote
25	114	4.1	424	2	A10465	probable glycerol-
26	114	4.1	1066	2	G84746	hypothetical prote
27	113.5	4.1	943	2	F70873	acetic acid hydrat
28	111	4.0	1138	2	G71554	probable transmem
29	109.5	3.9	915	2	T12526	hypothetical prote
30	108.5	3.9	4273	2	C69679	polyketide synthas
31	108	3.9	623	2	S46427	botulinum neurotox
32	107.5	3.9	422	2	AG3323	threonine dehydrat
33	107.5	3.9	565	2	T26161	hypothetical prote
34	107.5	3.9	850	2	AE1954	hypothetical prote
35	107.5	3.9	2090	2	S26058	probable transform
36	107.5	3.9	3535	2	E83641	probable hemagglut
37	106	3.8	354	2	E71193	probable operon pr
38	106	3.8	619	2	C70669	probable acyl-CoA
39	106	3.8	1169	2	S38181	flocculation prote
40	105.5	3.8	662	2	E97016	transketolase (imp
41	105.5	3.8	887	2	D82049	phosphoenolpyruvat
42	105.5	3.8	898	1	DJBPT4	DNA-directed DNA p
43	105.5	3.8	1097	2	S17308	leukemia inhibitor
44	105	3.8	2440	2	S39162	transcription coac
45	104.5	3.8	422	2	AH1694	threonine dehydrat

ALIGNMENTS

RESULT 1
A33879
aminopeptidase ysc1 (EC 3.4.11.-) precursor, vacuolar - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein YK103c; protein YK1455
C/Species: Saccharomyces cerevisiae
C/Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C/Accession: A33879; B33879; S39101; S37930; S25400
R/Chang, Y.H.; Smith, J.A.
J. Biol. Chem. 264, 6979-6983, 1989
A/Title: Molecular cloning and sequencing of genomic DNA encoding aminopeptidase I fro
A/Reference number: A33879; NCBI:89214116; PMID:2651436
A/Accession: A33879
A/Molecule type: DNA
A/Residues: 1-514 <CHA>
A/Cross-references: UNIPROT:P14904; EMBL:M25548; NID:G295617; PIDN:AAA34738.1; PID:G29
A/Accession: B33879
A/Molecule type: protein
A/Residues: 46-63 <CH2>
R/Cheret, G.; Pallier, C.; Valens, M.; Daigman-Formier, B.; Fukuhara, H.; Bojotin-Fuku
Yeast 9, 1259-1265, 1993
A/Title: The DNA sequence analysis of the HAP4-LAP4 region on chromosome XI of Sacchar
A/Reference number: S39094; NCBI:94152173; PMID:8109175
A/Accession: S39101
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-514 <CH2>
A/Cross-references: EMBL:X71133; NID:G411205; PIDN:CAA50454.1; PID:G411213
A/Experimental source: strain S288C
R/Cheret, G.; Fukuhara, H.; Bojotin-Fukuhara, M.; Daigman-Formier, B.; Pallier, C.; Fu
Submitted to the Protein Sequence Database, March 1994
A/Reference number: S37920
A/Accession: S37930
A/Molecule type: DNA
A/Residues: 1-514 <CH2>
A/Cross-references: EMBL:Z28103; NID:G486172; PIDN:CAA81943.1; PID:G486173; MIPS:YK110
A/Experimental source: strain S288C
R/Cueva, R.; Garcia-Alvarez, N.; Suarez-Rendueles, P.
PDBS Lett. 259, 125-129, 1989